

61835-3.ST25.txt
SEQUENCE LISTING

<110> Vanaja, Donkena Krishna
Young, Charles Y.F.

<120> Methods And Compositions For Diagnosis, Staging and Prognosis of
Prostate Cancer

<130> 61835-3

<150> US 60/487,553

<151> 2003-07-14

<150> PCT/US2004/022850

<151> 2004-07-14

<160> 52

<170> PatentIn version 3.3

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<212> DNA

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Asp Cys Pro Lys Ile Thr Leu Glu His Leu Gly Ile Cys Cys His Glu
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Tyr Cys Phe Lys Cys Gly Ile Cys Ser Lys Pro Met Gly Asp Leu Leu
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                                   1           5

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Val Val Ile Phe Ala Thr Phe Val Thr Leu Cys Asn Ala Ser Cys Tyr
      10           15           20

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Phe Ile Pro Asn Glu Gly Val Pro Gly Asp Ser Thr Arg Lys Cys Met
      25           30           35

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Asp Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp
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Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu Ile Ser Cys Cys Thr
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Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val Glu Lys Lys Asp Pro
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 35 40 45

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Thr Glu Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp
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      Met Ser Ser Glu Cys Asp Gly Gly Ser Lys Ala Val Met
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Asn Gly Leu Ala Pro Gly Ser Asn Gly Gln Asp Lys Asp Met Asp Pro
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Arg Gln His Glu Ser Lys Pro Gly Leu Glu Pro Glu Pro Ser Ser Ala
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Asp Glu Trp Arg Leu Ser Ser Ser Ala Asp Ala Asn Gly Asn Ala Gln
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Pro Ser Ser Leu Ala Ala Lys Gly Tyr Arg Ser Val His Pro Asn Leu
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Pro Ser Asp Lys Ser Gln Asp Ala Thr Ser Ser Ser Ala Ala Gln Pro
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Glu Val Ile Val Val Pro Leu Tyr Leu Val Asn Thr Asp Arg Gly Gln
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Glu Gly Thr Ala Arg Pro Pro Thr Pro Leu Gly Pro Leu Gly Cys Val
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Pro Thr Ile Pro Ala Thr Ala Ser Ala Ala Ser Pro Leu Thr Phe Pro
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Thr Leu Asp Asp Phe Ile Pro Pro His Leu Gln Arg Trp Pro His His
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Asp Leu Arg Arg Val Ser Glu Pro Asp Leu Thr Gly Ala Val Ser Ser	
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acc gat tcc agt cct cta cta aat gaa gtt tct tct tcc ctt att gga	949
Thr Asp Ser Ser Pro Leu Leu Asn Glu Val Ser Ser Ser Leu Ile Gly	
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act gat tcc caa gcc ttt cca tca gtt agc aag cct tca tcc gcc tat	997
Thr Asp Ser Ser Gln Ala Phe Pro Ser Val Ser Lys Pro Ser Ser Ala Tyr	
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Pro Ser Thr Thr Ile Val Asn Pro Thr Ile Val Leu Leu Gln His Asn	
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Met Phe Lys Gln Ile His Lys Leu Asn Arg Asp Asp Asp Ser Asp Leu	
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Tyr Ser Pro Arg Tyr Ser Phe Ser Glu Asp Thr Lys Ser Pro Leu Ser	
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Val Lys Arg Ser Ala Thr Leu Pro Leu Pro Ala Arg Ser Ser Ser Leu	
415 420 425	
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Lys Ser Ser Ser Glu Arg Asn Asp Trp Glu Pro Pro Asp Lys Lys Val	

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Arg	Arg	Thr	Lys	Gln	Phe	Gly	Thr	Phe	Pro	Gly	Asn	Tyr	Val	Lys	Pro		2629
		800					805					810					
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Leu	Tyr	Leu															2681
		815															
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																	3221
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																	3281

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<400> 33

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Cys Thr Gly Lys Gly Ala Val Thr Leu Arg Ala Ser Ser Ser Tyr Arg
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Glu Thr Pro Ser Ser Ser Pro Ala Ser Pro Gln Glu Thr Arg Gln His
 50 55 60

Glu Ser Lys Pro Gly Leu Glu Pro Glu Pro Ser Ser Ala Asp Glu Trp
 65 70 75 80

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Arg Leu Ser Ser Ser Ala Asp Ala Asn Gly Asn Ala Gln Pro Ser Ser
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Leu Ala Ala Lys Gly Tyr Arg Ser Val His Pro Asn Leu Pro Ser Asp
 100 105 110

Lys Ser Gln Asp Ala Thr Ser Ser Ser Ala Ala Gln Pro Glu Val Ile
 115 120 125

Val Val Pro Leu Tyr Leu Val Asn Thr Asp Arg Gly Gln Glu Gly Thr
 130 135 140

Ala Arg Pro Pro Thr Pro Leu Gly Pro Leu Gly Cys Val Pro Thr Ile
 145 150 155 160

Pro Ala Thr Ala Ser Ala Ala Ser Pro Leu Thr Phe Pro Thr Leu Asp
 165 170 175

Asp Phe Ile Pro Pro His Leu Gln Arg Trp Pro His His Ser Gln Pro
 180 185 190

Ala Arg Ala Ser Gly Ser Phe Ala Pro Ile Ser Gln Thr Pro Pro Ser
 195 200 205

Phe Ser Pro Pro Pro Pro Leu Val Pro Pro Ala Pro Glu Asp Leu Arg
 210 215 220

Arg Val Ser Glu Pro Asp Leu Thr Gly Ala Val Ser Ser Thr Asp Ser
 225 230 235 240

Ser Pro Leu Leu Asn Glu Val Ser Ser Ser Leu Ile Gly Thr Asp Ser
 245 250 255

Gln Ala Phe Pro Ser Val Ser Lys Pro Ser Ser Ala Tyr Pro Ser Thr
 260 265 270

Thr Ile Val Asn Pro Thr Ile Val Leu Leu Gln His Asn Arg Glu Gln
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Gln Lys Arg Leu Ser Ser Leu Ser Asp Pro Val Ser Glu Arg Arg Val
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Gly Glu Gln Asp Ser Ala Pro Thr Gln Glu Lys Pro Thr Ser Pro Gly
 305 310 315 320

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Lys Ala Ile Glu Lys Arg Ala Lys Asp Asp Ser Arg Arg Val Val Lys
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Ser Thr Gln Asp Leu Ser Asp Val Ser Met Asp Glu Val Gly Ile Pro
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Leu Arg Asn Thr Glu Arg Ser Lys Asp Trp Tyr Lys Thr Met Phe Lys
 355 360 365

Gln Ile His Lys Leu Asn Arg Asp Asp Asp Ser Asp Leu Tyr Ser Pro
 370 375 380

Arg Tyr Ser Phe Ser Glu Asp Thr Lys Ser Pro Leu Ser Val Pro Arg
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Ser Lys Ser Glu Met Ser Tyr Ile Asp Gly Glu Lys Val Val Lys Arg
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Ser Ala Thr Leu Pro Leu Pro Ala Arg Ser Ser Ser Leu Lys Ser Ser
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Ser Glu Arg Asn Asp Trp Glu Pro Pro Asp Lys Lys Val Asp Thr Arg
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Lys Tyr Arg Ala Glu Pro Lys Ser Ile Tyr Glu Tyr Gln Pro Gly Lys
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Ser Ser Val Leu Thr Asn Glu Lys Met Ser Ser Ala Ile Ser Pro Thr
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Pro Glu Ile Ser Ser Glu Thr Pro Gly Tyr Ile Tyr Ser Ser Asn Phe
 485 490 495

His Ala Val Lys Arg Glu Ser Asp Gly Ala Pro Gly Asp Leu Thr Ser
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Leu Glu Asn Glu Arg Gln Ile Tyr Lys Ser Val Leu Glu Gly Gly Asp
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Ile Pro Leu Gln Gly Leu Ser Gly Leu Lys Arg Pro Ser Ser Ser Ala
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Ser Thr Lys Asp Ser Glu Ser Pro Arg His Phe Ile Pro Ala Asp Tyr
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Leu Glu Ser Thr Glu Glu Phe Ile Arg Arg Arg His Asp Asp Lys Glu
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Met Arg Pro Ala Arg Ala Lys Phe Asp Phe Lys Ala Gln Thr Leu Lys
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Asp Gln Asn Trp Tyr Glu Gly Glu His His Gly Arg Val Gly Ile Phe
610 615 620

Pro Arg Thr Tyr Ile Glu Leu Leu Pro Pro Ala Glu Lys Ala Gln Pro
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Lys Lys Leu Thr Pro Val Gln Val Leu Glu Tyr Gly Glu Ala Ile Ala
645 650 655

Lys Phe Asn Phe Asn Gly Asp Thr Gln Val Glu Met Ser Phe Arg Lys
660 665 670

Gly Glu Arg Ile Thr Leu Leu Arg Gln Val Asp Glu Asn Trp Tyr Glu
675 680 685

Gly Arg Ile Pro Gly Thr Ser Arg Gln Gly Ile Phe Pro Ile Thr Tyr
690 695 700

Val Asp Val Ile Lys Arg Pro Leu Val Lys Asn Pro Val Asp Tyr Met
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Asp Leu Pro Phe Ser Ser Ser Pro Ser Arg Ser Ala Thr Ala Ser Pro
725 730 735

Gln Gln Pro Gln Ala Gln Gln Arg Arg Val Thr Pro Asp Arg Ser Gln
740 745 750

Thr Ser Gln Asp Leu Phe Ser Tyr Gln Ala Leu Tyr Ser Tyr Ile Pro
755 760 765

Gln Asn Asp Asp Glu Leu Glu Leu Arg Asp Gly Asp Ile Val Asp Val
770 775 780

Met Glu Lys Cys Asp Asp Gly Trp Phe Val Gly Thr Ser Arg Arg Thr

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Gly Arg Ser Asn Glu Glu Glu Glu Thr Ser Asp Ser Ser Leu Glu Lys	
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caa act cga tcc aaa tac tgc aca gaa acc tcc ggt gtc cac ggt gac	355
Gln Thr Arg Ser Lys Tyr Cys Thr Glu Thr Ser Gly Val His Gly Asp	
70 75 80 85	
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Ser Pro Tyr Gly Ser Gly Thr Met Asp Thr His Ser Leu Glu Ser Lys	
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Ala Glu Arg Ile Ala Arg Tyr Lys Ala Glu Arg Arg Arg Gln Leu Ala	
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Glu Lys Tyr Gly Leu Thr Leu Asp Pro Glu Ala Asp Ser Glu Tyr Leu	
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Ser Arg Tyr Thr Lys Ser Arg Lys Glu Pro Asp Ala Val Glu Lys Arg	
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Gly Gly Lys Ser Asp Lys Gln Glu Glu Ser Ser Arg Asp Ala Ser Ser	
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Leu Tyr Pro Gly Thr Glu Thr Met Gly Leu Arg Thr Cys Ala Gly Glu	
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Ser Lys Asp Tyr Ala Leu His Val Gly Asp Gly Ser Ser Asp Pro Glu	
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Val Leu Leu Asn Ile Glu Asn Gln Arg Arg Gly Gln Glu Leu Ser Ala	
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Thr Arg Gln Ala His Asp Leu Ser Pro Ala Ala Glu Ser Ser Ser Thr	
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Phe Ser Phe Ser Gly Arg Asp Ser Ser Phe Thr Glu Val Pro Arg Ser	
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Pro Lys His Ala His Ser Ser Ser Leu Gln Gln Ala Ala Ser Arg Ser	
250 255 260	
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Pro Ser Phe Gly Asp Pro Gln Leu Ser Pro Glu Ala Arg Pro Arg Cys	
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Glu Arg Ala Lys Leu Ser Val Ala Ala Lys Arg Leu Leu Phe Arg Glu	
295 300 305	
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Met Glu Lys Ser Phe Asp Glu Gln Asn Val Pro Lys Arg Arg Ser Arg	
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Thr Gln Pro Ile Thr Thr Glu Glu Val Val Ile Ala Ala Thr Leu Gln	
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Lys Glu Leu Ala Glu Gln Gly Glu Pro Asp Ser Ser Thr Leu Ser Leu	
375 380 385	
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Ala Glu Lys Leu Ala Leu Phe Asn Lys Leu Ser Gln Pro Val Ser Lys	
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Ala Arg Tyr Gln Thr Gln Pro Val Thr Leu Gly Glu Val Glu Gln Val	
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Gln Ser Gly Lys Leu Ile Pro Phe Ser Pro Ala Val Asn Thr Ser Val	
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Ser Thr Val Ala Ser Thr Val Ala Pro Met Tyr Ala Gly Asp Leu Arg	
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Thr Lys Pro Pro Leu Asp His Asn Ala Ser Ala Thr Asp Tyr Lys Phe	
470 475 480 485	
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490 495 500	
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Ser Gln Ala Trp Gln Pro Leu Val Glu Gly Ser Glu Asn Lys Gly Met	

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Asp	Ser	Gly	Met	Glu	Lys	Tyr	Gly	Ser	Phe	Glu	Glu	Ala	Glu	Ala	Ser	
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Tyr	Pro	Ile	Leu	Asn	Arg	Ala	Arg	Glu	Gly	Asp	Ser	His	Lys	Glu	Ser	
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Gly	Arg	Met	Val	Lys	Lys	Gly	Leu	Ala	Ser	Pro	Thr	Ala	Ile	Thr	Pro	
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gta	gcc	tca	gcc	att	tgc	ggt	aaa	aca	aga	ggc	acc	aca	ccc	gtt	tcc	2563
Val	Ala	Ser	Ala	Ile	Cys	Gly	Lys	Thr	Arg	Gly	Thr	Thr	Pro	Val	Ser	
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Lys	Pro	Leu	Glu	Asp	Ile	Glu	Ala	Arg	Pro	Asp	Met	Gln	Leu	Glu	Ser	
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Lys	Val	Gly	Gly	Met	His	Glu	Thr	Val	Leu	Thr	Val	Thr	Gly	Lys	Ser	
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Tyr	Arg	Ser	Val	Asp	Tyr	Asn	Met	Pro	Arg	Ser	Pro	Val	Glu	Met	Asp	
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Glu	Asp	Phe	Asp	Val	Ile	Phe	Asp	Pro	Tyr	Ala	Pro	Lys	Leu	Thr	Ser	
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gcc	tcc	aaa	aac	ccc	ctg	aaa	atg	ctg	gcg	gca	aga	gaa	gat	ctc	ctt	2947
Ala	Ser	Lys	Asn	Pro	Leu	Lys	Met	Leu	Ala	Ala	Arg	Glu	Asp	Leu	Leu	
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cgg agc gtc aac ctg acg gaa cag aac tct aac aac agc gcc gtg	3136
Arg Ser Val Asn Leu Thr Glu Gln Asn Ser Asn Asn Ser Ala Val	
1000 1005 1010	
ccc tac aag agg ctg atg ctg ttg cag att aaa gga aga aga cat	3181
Pro Tyr Lys Arg Leu Met Leu Leu Gln Ile Lys Gly Arg Arg His	
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Val Glu Gly	His Asp Arg Arg Gln	Phe Glu Ile Thr Ser	Val Ser	
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735

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1625

1630

1635

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61835-3.ST25.txt

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 tggagg 2039

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 <212> PRT
 <213> homo sapiens

<400> 39

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20 25 30

Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Tyr Lys Ser Tyr Val
35 40 45

Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile Leu Leu
50 55 60

Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met Thr
65 70 75 80

Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu Leu
85 90 95

Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro Leu
100 105 110

Lys Arg Tyr Ala His Ala Leu Val Phe Gly Ile Leu Leu Thr Cys Arg
115 120 125

Leu Leu Ile Ala Arg Lys Pro Glu Asp Arg Ser Ser Glu Lys Lys Pro
130 135 140

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Gln Gly Lys Val Lys Val Ser
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 <213> homo sapiens

<220>
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 Met Tyr Ser Glu Ile Gln Arg Glu Arg Ala Asp Ile
 1 5 10
 ggg ggc ctg atg gcc cgg cca gaa tac aga gag tgg aat ccg gag ctc 158
 Gly Gly Leu Met Ala Arg Pro Glu Tyr Arg Glu Trp Asn Pro Glu Leu
 15 20 25
 atc aag ccc aag aag ctg ctg aac ccc gtg aag gcc tct cgg agt cac 206
 Ile Lys Pro Lys Lys Leu Leu Asn Pro Val Lys Ala Ser Arg Ser His
 30 35 40
 cag gag ctc cac cgg gag ctg ctc atg aac cac aga agg ggc ctt ggt 254
 Gln Glu Leu His Arg Glu Leu Leu Met Asn His Arg Arg Gly Leu Gly
 45 50 55 60
 gtg gac agc aag cca gag ctg cag cgt gtc cta gag cac cgc cgg cgg 302
 Val Asp Ser Lys Pro Glu Leu Gln Arg Val Leu Glu His Arg Arg Arg
 65 70 75
 aac cag ctc atc aag aag aag aag gag gag ctg gaa gcc aag cgg ctg 350
 Asn Gln Leu Ile Lys Lys Lys Lys Glu Glu Leu Glu Ala Lys Arg Leu
 80 85 90
 cag tgc ccc ttt gag cag gag ctg ctg aga cgg cag cag agg ctg aac 398
 Gln Cys Pro Phe Glu Gln Glu Leu Leu Arg Arg Gln Gln Arg Leu Asn
 95 100 105
 cag ctg gaa aaa cca cca gag aag gaa gag gat cac gcc ccc gag ttt 446
 Gln Leu Glu Lys Pro Pro Glu Lys Glu Glu Asp His Ala Pro Glu Phe
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 Ile Lys Val Arg Glu Asn Leu Arg Arg Ile Ala Thr Leu Thr Ser Glu
 125 130 135 140
 gag aga gag ctg tag ggccagctgc cgggctcagg ccaactgccca ccttggcctg 549
 Glu Arg Glu Leu
 gacagcctcc ttcagccctt ctgtacctgg cagccctggg cccagggccc tgggacgtct 609
 gtgatgttcc cacctgcttc tgtagaaatg tgtcacccca gagggcctgg ctctccctgg 669
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61835-3.ST25.txt

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ggcagaattg aggaggaaga ggtggccctc tgacttgaca agccttctgt tctgcccagg 849
ccttcccacc aggaatctcc gaggtcccc agggccccgc ttctccgtac accccagctc 909
ctaggtctca gagaactccc ccacctgtgg ttttacctgc agccagcaga gcttagcttc 969
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<210> 41
<211> 144
<212> PRT
<213> homo sapiens

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<400> 41
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1           5           10           15

```

```

Ala Arg Pro Glu Tyr Arg Glu Trp Asn Pro Glu Leu Ile Lys Pro Lys
          20           25           30

```

```

Lys Leu Leu Asn Pro Val Lys Ala Ser Arg Ser His Gln Glu Leu His
          35           40           45

```

```

Arg Glu Leu Leu Met Asn His Arg Arg Gly Leu Gly Val Asp Ser Lys
          50           55           60

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Pro Glu Leu Gln Arg Val Leu Glu His Arg Arg Arg Asn Gln Leu Ile
65           70           75           80

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61835-3.ST25.txt

Lys Lys Lys Lys Glu Glu Leu Glu Ala Lys Arg Leu Gln Cys Pro Phe
85 90 95

Glu Gln Glu Leu Leu Arg Arg Gln Gln Arg Leu Asn Gln Leu Glu Lys
100 105 110

Pro Pro Glu Lys Glu Glu Asp His Ala Pro Glu Phe Ile Lys Val Arg
115 120 125

Glu Asn Leu Arg Arg Ile Ala Thr Leu Thr Ser Glu Glu Arg Glu Leu
130 135 140

<210> 42
<211> 228
<212> DNA
<213> homo sapiens

<400> 42
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agttctcaga gtgagaatag ctgaatacag gttcactgtg aaaaaaag 228

<210> 43
<211> 2797
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (351)..(1775)

<400> 43
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ggaactataa ctctctgcg agaggcggag aactccttcc ccaaattctt tggggacttt 180
tctctcttta ccacactccg cccctgagag gagttgaggg gccagttcgg ccgccgcgcg 240
cgtcttcccg ttcggcgtgt gcttgccccg gggaaccggg agggcccggc gatcgcgcg 300
cggccgccgc gaggggtgtga gcgcgcgtgg gcgcccgcgc agccgaggcc atg gtg 356
Met Val
1
cag caa acc aac aat gcc gag aac acg gaa gcg ctg ctg gcc ggc gag 404

61835-3.ST25.txt

Gln	Gln	Thr	Asn	Asn	Ala	Glu	Asn	Thr	Glu	Ala	Leu	Leu	Ala	Gly	Glu	
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Ser	Ser	Asp	Ser	Gly	Ala	Gly	Leu	Glu	Leu	Gly	Ile	Ala	Ser	Ser	Pro	
	20					25					30					
acg	ccc	ggc	tcc	acc	gcc	tcc	acg	ggc	ggc	aag	gcc	gac	gac	ccg	agc	500
Thr	Pro	Gly	Ser	Thr	Ala	Ser	Thr	Gly	Gly	Lys	Ala	Asp	Asp	Pro	Ser	
35					40					45					50	
tgg	tgc	aag	acc	ccg	agt	ggg	cac	atc	aag	cga	ccc	atg	aac	gcc	ttc	548
Trp	Cys	Lys	Thr	Pro	Ser	Gly	His	Ile	Lys	Arg	Pro	Met	Asn	Ala	Phe	
				55					60					65		
atg	gtg	tgg	tcg	cag	atc	gag	cgg	cgc	aag	atc	atg	gag	cag	tcg	ccc	596
Met	Val	Trp	Ser	Gln	Ile	Glu	Arg	Arg	Lys	Ile	Met	Glu	Gln	Ser	Pro	
			70					75					80			
gac	atg	cac	aac	gcc	gag	atc	tcc	aag	cgg	ctg	ggc	aaa	cgc	tgg	aag	644
Asp	Met	His	Asn	Ala	Glu	Ile	Ser	Lys	Arg	Leu	Gly	Lys	Arg	Trp	Lys	
		85					90					95				
ctg	ctc	aaa	gac	agc	gac	aag	atc	cct	ttc	att	cga	gag	gcg	gag	cgg	692
Leu	Leu	Lys	Asp	Ser	Asp	Lys	Ile	Pro	Phe	Ile	Arg	Glu	Ala	Glu	Arg	
	100					105					110					
ctg	cgc	ctc	aag	cac	atg	gct	gac	tac	ccc	gac	tac	aag	tac	cgg	ccc	740
Leu	Arg	Leu	Lys	His	Met	Ala	Asp	Tyr	Pro	Asp	Tyr	Lys	Tyr	Arg	Pro	
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agg	aag	aag	gtg	aag	tcc	ggc	aac	gcc	aac	tcc	agc	tcc	tcg	gcc	gcc	788
Arg	Lys	Lys	Val	Lys	Ser	Gly	Asn	Ala	Asn	Ser	Ser	Ser	Ser	Ala	Ala	
				135					140					145		
gcc	tcc	tcc	aag	ccg	ggg	gag	aag	gga	gac	aag	gtc	ggt	ggc	agt	ggc	836
Ala	Ser	Ser	Lys	Pro	Gly	Glu	Lys	Gly	Asp	Lys	Val	Gly	Gly	Ser	Gly	
			150					155					160			
ggg	ggc	ggc	cat	ggg	ggc	ggc	ggc	ggc	ggc	ggg	agc	agc	aac	gcg	ggg	884
Gly	Gly	Gly	His	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Ser	Asn	Ala	Gly	
		165					170					175				
gga	gga	ggc	ggc	ggt	gcg	agt	ggc	ggc	ggc	gcc	aac	tcc	aaa	ccg	gcg	932
Gly	Gly	Gly	Gly	Gly	Ala	Ser	Gly	Gly	Gly	Ala	Asn	Ser	Lys	Pro	Ala	
	180					185					190					
cag	aaa	aag	agc	tgc	ggc	tcc	aaa	gtg	gcg	ggc	ggc	gcg	ggc	ggt	ggg	980
Gln	Lys	Lys	Ser	Cys	Gly	Ser	Lys	Val	Ala	Gly	Gly	Ala	Gly	Gly	Gly	
195					200					205					210	
gtt	agc	aaa	ccg	cac	gcc	aag	ctc	atc	ctg	gca	ggc	ggc	ggc	ggc	ggc	1028
Val	Ser	Lys	Pro	His	Ala	Lys	Leu	Ile	Leu	Ala	Gly	Gly	Gly	Gly	Gly	
				215					220					225		
ggg	aaa	gca	gcg	gct	gcc	gcc	gcc	gcc	tcc	ttc	gcc	gcc	gaa	cag	gcg	1076
Gly	Lys	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ser	Phe	Ala	Ala	Glu	Gln	Ala	
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ctg tac aag gcg cgg act ccc agc gcc tcg gcc tcc gcc tcc tcg gca Leu Tyr Lys Ala Arg Thr Pro Ser Ala Ser Ala Ser Ser Ser Ala 260 265 270	1172
gcc tcg gcc tcc gca gcg ctc gcg gcc ccg ggc aag cac ctg gcg gag Ala Ser Ala Ser Ala Ala Leu Ala Ala Pro Gly Lys His Leu Ala Glu 275 280 285 290	1220
aag aag gtg aag cgc gtc tac ctg ttc ggc ggc ctg ggc acg tcg tcg Lys Lys Val Lys Arg Val Tyr Leu Phe Gly Gly Leu Gly Thr Ser Ser 295 300 305	1268
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ggc ctg tac gag gag gag ggc gcg ggc tgc tcg ccc gac gcg ccc agc Gly Leu Tyr Glu Glu Glu Gly Ala Gly Cys Ser Pro Asp Ala Pro Ser 325 330 335	1364
ctg agc ggc cgc agc agc gcc gcc tcg tcc ccc gcc gcc ggc cgc tcg Leu Ser Gly Arg Ser Ser Ala Ala Ser Ser Pro Ala Ala Gly Arg Ser 340 345 350	1412
ccc gcc gac cac cgc ggc tac gcc agc ctg cgc gcc gcc tcg ccc gcc Pro Ala Asp His Arg Gly Tyr Ala Ser Leu Arg Ala Ala Ser Pro Ala 355 360 365 370	1460
ccg tcc agc gcg ccc tcg cac gcg tcc tcc tcg gcc tcg tcc cac tcc Pro Ser Ser Ala Pro Ser His Ala Ser Ser Ser Ala Ser Ser His Ser 375 380 385	1508
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gac gac ctg ctc gac ctg aac ccc agc tca aac ttt gag agc atg tcc Asp Asp Leu Leu Asp Leu Asn Pro Ser Ser Asn Phe Glu Ser Met Ser 405 410 415	1604
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aac ttc gag ccc ggc tcc ggc tcg cac ttc gag ttc ccg gac tac tgc Asn Phe Glu Pro Gly Ser Gly Ser His Phe Glu Phe Pro Asp Tyr Cys 435 440 445 450	1700
acg ccc gag gtg agc gag atg atc tcg gga gac tgg ctc gag tcc agc Thr Pro Glu Val Ser Glu Met Ile Ser Gly Asp Trp Leu Glu Ser Ser 455 460 465	1748
atc tcc aac ctg gtt ttc acc tac tga agggcgcgca ggcagggaga Ile Ser Asn Leu Val Phe Thr Tyr 470	1795

61835-3.ST25.txt

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<210> 44
<211> 474
<212> PRT
<213> homo sapiens

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<400> 44

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1          5          10          15

```

```

Gly Glu Ser Ser Asp Ser Gly Ala Gly Leu Glu Leu Gly Ile Ala Ser
20          25          30

```

```

Ser Pro Thr Pro Gly Ser Thr Ala Ser Thr Gly Gly Lys Ala Asp Asp
35          40          45

```

```

Pro Ser Trp Cys Lys Thr Pro Ser Gly His Ile Lys Arg Pro Met Asn
50          55          60

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61835-3.ST25.txt

Ala Phe Met Val Trp Ser Gln Ile Glu Arg Arg Lys Ile Met Glu Gln
 65 70 75 80

Ser Pro Asp Met His Asn Ala Glu Ile Ser Lys Arg Leu Gly Lys Arg
 85 90 95

Trp Lys Leu Leu Lys Asp Ser Asp Lys Ile Pro Phe Ile Arg Glu Ala
 100 105 110

Glu Arg Leu Arg Leu Lys His Met Ala Asp Tyr Pro Asp Tyr Lys Tyr
 115 120 125

Arg Pro Arg Lys Lys Val Lys Ser Gly Asn Ala Asn Ser Ser Ser Ser
 130 135 140

Ala Ala Ala Ser Ser Lys Pro Gly Glu Lys Gly Asp Lys Val Gly Gly
 145 150 155 160

Ser Gly Gly Gly Gly His Gly Gly Gly Gly Gly Gly Gly Ser Ser Asn
 165 170 175

Ala Gly Gly Gly Gly Gly Gly Ala Ser Gly Gly Gly Ala Asn Ser Lys
 180 185 190

Pro Ala Gln Lys Lys Ser Cys Gly Ser Lys Val Ala Gly Gly Ala Gly
 195 200 205

Gly Gly Val Ser Lys Pro His Ala Lys Leu Ile Leu Ala Gly Gly Gly
 210 215 220

Gly Gly Gly Lys Ala Ala Ala Ala Ala Ala Ser Phe Ala Ala Glu
 225 230 235 240

Gln Ala Gly Ala Ala Ala Leu Leu Pro Leu Gly Ala Ala Ala Asp His
 245 250 255

His Ser Leu Tyr Lys Ala Arg Thr Pro Ser Ala Ser Ala Ser Ala Ser
 260 265 270

Ser Ala Ala Ser Ala Ser Ala Ala Leu Ala Ala Pro Gly Lys His Leu
 275 280 285

Ala Glu Lys Lys Val Lys Arg Val Tyr Leu Phe Gly Gly Leu Gly Thr
 290 295 300

61835-3.ST25.txt

Ser Ser Ser Pro Val Gly Gly Val Gly Ala Gly Ala Asp Pro Ser Asp
305 310 315 320

Pro Leu Gly Leu Tyr Glu Glu Glu Gly Ala Gly Cys Ser Pro Asp Ala
325 330 335

Pro Ser Leu Ser Gly Arg Ser Ser Ala Ala Ser Ser Pro Ala Ala Gly
340 345 350

Arg Ser Pro Ala Asp His Arg Gly Tyr Ala Ser Leu Arg Ala Ala Ser
355 360 365

Pro Ala Pro Ser Ser Ala Pro Ser His Ala Ser Ser Ser Ala Ser Ser
370 375 380

His Ser Ser Ser Ser Ser Ser Ser Gly Ser Ser Ser Ser Asp Asp Glu
385 390 395 400

Phe Glu Asp Asp Leu Leu Asp Leu Asn Pro Ser Ser Asn Phe Glu Ser
405 410 415

Met Ser Leu Gly Ser Phe Ser Ser Ser Ser Ala Leu Asp Arg Asp Leu
420 425 430

Asp Phe Asn Phe Glu Pro Gly Ser Gly Ser His Phe Glu Phe Pro Asp
435 440 445

Tyr Cys Thr Pro Glu Val Ser Glu Met Ile Ser Gly Asp Trp Leu Glu
450 455 460

Ser Ser Ile Ser Asn Leu Val Phe Thr Tyr
465 470

<210> 45
<211> 1334
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (14)..(601)

<400> 45
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Met Gly Ser Gln Ser Ser Lys Ala Pro Arg Gly Asp
1 5 10

49

61835-3.ST25.txt

gtg acc gcc gag gag gca gca ggc gct tcc ccc gcg aag gcc aac ggc Val Thr Ala Glu Glu Ala Ala Gly Ala Ser Pro Ala Lys Ala Asn Gly 15 20 25	97
cag gag aat ggc cac gtg aaa agc aat gga gac tta tcc ccc aag ggt Gln Glu Asn Gly His Val Lys Ser Asn Gly Asp Leu Ser Pro Lys Gly 30 35 40	145
gaa ggg gag tcg ccc cct gtg aac gga aca gat gag gca gcc ggg gcc Glu Gly Glu Ser Pro Pro Val Asn Gly Thr Asp Glu Ala Ala Gly Ala 45 50 55 60	193
act ggc gat gcc atc gag cca gca ccc cct agc cag ggt gct gag gcc Thr Gly Asp Ala Ile Glu Pro Ala Pro Pro Ser Gln Gly Ala Glu Ala 65 70 75	241
aag ggg gag gtc ccc ccc aag gag acc ccc aag aag aag aag aaa ttc Lys Gly Glu Val Pro Pro Lys Glu Thr Pro Lys Lys Lys Lys Lys Phe 80 85 90	289
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cgg aag gag ggt ggg ggt gat tct tct gcc tcc tca ccc aca gag gaa Arg Lys Glu Gly Gly Gly Asp Ser Ser Ala Ser Ser Pro Thr Glu Glu 110 115 120	385
gag cag gag cag ggg gag atc ggt gcc tgc agc gac gag ggc act gct Glu Gln Glu Gln Gly Glu Ile Gly Ala Cys Ser Asp Glu Gly Thr Ala 125 130 135 140	433
cag gaa ggg aag gcc gca gcc acc cct gag agc cag gaa ccc cag gcc Gln Glu Gly Lys Ala Ala Ala Thr Pro Glu Ser Gln Glu Pro Gln Ala 145 150 155	481
aag ggg gca gag gct agt gca gcc tca gaa gaa gag gca ggg ccc cag Lys Gly Ala Glu Ala Ser Ala Ala Ser Glu Glu Glu Ala Gly Pro Gln 160 165 170	529
gct aca gag cca tcc act ccc tcg ggg ccg gag agt ggc cct aca cca Ala Thr Glu Pro Ser Thr Pro Ser Gly Pro Glu Ser Gly Pro Thr Pro 175 180 185	577
gcc agc gct gag cag aat gag tag ctaggtaggg gcaggtgggt gatctctaag Ala Ser Ala Glu Gln Asn Glu 190 195	631
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tcccttacag cttcccaagt taggttagtg atgtgaaatg ctctgtccc tggccctacc	871
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61835-3.ST25.txt

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caagtagggtt ttgtttaccc tactcccca atccctgagc cagaagtggg gtgcttatac   991
tcccaaacct tgagtgtcca gccttccctt gttgttttta gtctcttggtg ctgtgcctag  1051
tggcacctgg gctggggagg aactgcccc gtctagggtt ttataaatgt cttactcaag   1111
ttcaaacctc cagcctgtga atcaactgtg tctctttttt gacttggtaa gcaagtatta   1171
ggctttgggg tggggggagg tctgtaattg gaaacaactt cttgtctttt tttctccac   1231
tgttgtaaat aacttttaat ggccaaaccc cagatttgta cttttttttt ttttctaact   1291
gctaaaacca ttctcttcca cctggtttta ctgtaacatt tgg                      1334

```

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<210> 46
<211> 195
<212> PRT
<213> homo sapiens

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<400> 46
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Met Gly Ser Gln Ser Ser Lys Ala Pro Arg Gly Asp Val Thr Ala Glu
1              5              10              15

```

```

Glu Ala Ala Gly Ala Ser Pro Ala Lys Ala Asn Gly Gln Glu Asn Gly
      20              25              30

```

```

His Val Lys Ser Asn Gly Asp Leu Ser Pro Lys Gly Glu Gly Glu Ser
      35              40              45

```

```

Pro Pro Val Asn Gly Thr Asp Glu Ala Ala Gly Ala Thr Gly Asp Ala
      50              55              60

```

```

Ile Glu Pro Ala Pro Pro Ser Gln Gly Ala Glu Ala Lys Gly Glu Val
65              70              75              80

```

```

Pro Pro Lys Glu Thr Pro Lys Lys Lys Lys Lys Phe Ser Phe Lys Lys
      85              90              95

```

```

Pro Phe Lys Leu Ser Gly Leu Ser Phe Lys Arg Asn Arg Lys Glu Gly
      100             105             110

```

```

Gly Gly Asp Ser Ser Ala Ser Ser Pro Thr Glu Glu Glu Gln Glu Gln
      115             120             125

```

```

Gly Glu Ile Gly Ala Cys Ser Asp Glu Gly Thr Ala Gln Glu Gly Lys
      130             135             140

```

```

Ala Ala Ala Thr Pro Glu Ser Gln Glu Pro Gln Ala Lys Gly Ala Glu

```

```

145                      150                      155                      160

Ala Ser Ala Ala Ser Glu Glu Glu Ala Gly Pro Gln Ala Thr Glu Pro
                      165                      170                      175

Ser Thr Pro Ser Gly Pro Glu Ser Gly Pro Thr Pro Ala Ser Ala Glu
                      180                      185                      190

Gln Asn Glu
                      195

<210> 47
<211> 662
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (49)..(456)

<400> 47
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                                   Met Ala Thr
                                   1

gtt cag cag ctg gaa gga aga tgg cgc ctg gtg gac agc aaa ggc ttt      105
Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser Lys Gly Phe
   5                      10                      15

gat gaa tac atg aag gag cta gga gtg gga ata gct ttg cga aaa atg      153
Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu Arg Lys Met
  20                      25                      30                      35

ggc gca atg gcc aag cca gat tgt atc atc act tgt gat ggt aaa aac      201
Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp Gly Lys Asn
                      40                      45                      50

ctc acc ata aaa act gag agc act ttg aaa aca aca cag ttt tct tgt      249
Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln Phe Ser Cys
                      55                      60                      65

acc ctg gga gag aag ttt gaa gaa acc aca gct gat ggc aga aaa act      297
Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly Arg Lys Thr
                      70                      75                      80

cag act gtc tgc aac ttt aca gat ggt gca ttg gtt cag cat cag gag      345
Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln His Gln Glu
                      85                      90                      95

tgg gat ggg aag gaa agc aca ata aca aga aaa ttg aaa gat ggg aaa      393
Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys Asp Gly Lys
  100                      105                      110                      115

tta gtg gtg gag tgt gtc atg aac aat gtc acc tgt act cgg atc tat      441

```

61835-3.ST25.txt

Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr Arg Ile Tyr
 120 125 130

gaa aaa gta gaa taa aaattccatc atcacttttg acaggagtta attaagagaa 496
 Glu Lys Val Glu
 135

tgaccaagct cagttcaatg agcaaatctc catactgttt ctttcttttt tttttcatta 556

ctgtgttcaa ttatctttat cataaacatt ttacatgcag ctatttcaaa gtgtgttgga 616

ttaattagga tcatcccttt ggtaataaaa taaatgtgtt tgtgct 662

<210> 48

<211> 135

<212> PRT

<213> homo sapiens

<400> 48

Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
 1 5 10 15

Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
 20 25 30

Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
 35 40 45

Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
 50 55 60

Phe Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
 65 70 75 80

Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
 85 90 95

His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys
 100 105 110

Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr
 115 120 125

Arg Ile Tyr Glu Lys Val Glu
 130 135

<210> 49

<211> 2808

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (80)..(610)

<400> 49

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                  Met Ser Ala Gly Gly Ala Ser Val Pro Pro Pro
                        1             5             10

ccg aac ccc gcc gtg tcc ttc ccg ccg ccc cgg gtc acc ctg ccc gcc      160
Pro Asn Pro Ala Val Ser Phe Pro Pro Pro Arg Val Thr Leu Pro Ala
                15             20             25

ggc ccc gac atc ctg cgg acc tac tgc gcc gcc ttc gtc tgc ctg gag      208
Gly Pro Asp Ile Leu Arg Thr Tyr Ser Gly Ala Phe Val Cys Leu Glu
                30             35             40

att ctg ttc ggg ggt ctt gtc tgg att ttg gtt gcc tcc tcc aat gtt      256
Ile Leu Phe Gly Gly Leu Val Trp Ile Leu Val Ala Ser Ser Asn Val
                45             50             55

cct cta cct cta cta caa gga tgg gtc atg ttt gtg tcc gtg aca gcg      304
Pro Leu Pro Leu Leu Gln Gly Trp Val Met Phe Val Ser Val Thr Ala
        60             65             70             75

ttt ttc ttt tgc ctc ctc ttt ctg ggc atg ttc ctc tct ggc atg gtg      352
Phe Phe Phe Ser Leu Leu Phe Leu Gly Met Phe Leu Ser Gly Met Val
                80             85             90

gct caa att gat gct aac tgg aac ttc ctg gat ttt gcc tac cat ttt      400
Ala Gln Ile Asp Ala Asn Trp Asn Phe Leu Asp Phe Ala Tyr His Phe
                95             100             105

aca gta ttt gtc ttc tat ttt gga gcc ttt tta ttg gaa gca gca gcc      448
Thr Val Phe Val Phe Tyr Phe Gly Ala Phe Leu Leu Glu Ala Ala Ala
                110             115             120

aca tcc ctg cat gat ttg cat tgc aat aca acc ata acc ggg cag cca      496
Thr Ser Leu His Asp Leu His Cys Asn Thr Thr Ile Thr Gly Gln Pro
                125             130             135

ctc ctg agt gat aac cag tat aac ata aac gta gca gcc tca att ttt      544
Leu Leu Ser Asp Asn Gln Tyr Asn Ile Asn Val Ala Ala Ser Ile Phe
        140             145             150             155

gcc ttt atg acg aca gct tgt tat ggt tgc agt ttg ggt ctg gct tta      592
Ala Phe Met Thr Thr Ala Cys Tyr Gly Cys Ser Leu Gly Leu Ala Leu
                160             165             170

cga aga tgg cga ccg taa cactccttag aaactggcag tcgtatgtta      640
Arg Arg Trp Arg Pro
                175

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61835-3.ST25.txt

gtttcacttg	tctactttat	atgtctgatc	aatttggata	ccattttgtc	cagatgcaaa	700
aacattccaa	aagtaatgtg	tttagtagag	agagactcta	agctcaagtt	ctggtttatt	760
tcattggatgg	aatgttaatt	ttattatgat	attaaagaaa	tggcctttta	ttttacatct	820
ctcccctttt	tccctttccc	cctttatttt	cctccttttc	tttctgaaag	tttcctttta	880
tgtccataaa	atacaaatat	attgttcata	aaaaattagt	atcccttttg	tttggttgct	940
gagtcacctg	aaccttaatt	ttaattggta	attacagccc	ctaaaaaaaa	cacatttcaa	1000
ataggcttcc	cactaaactc	tatattttag	tgtaaaccag	gaattggcac	acttttttta	1060
gaatgggcca	gatggtaaatt	atttatgctt	cacgggtccat	acagtctctg	tcacaactat	1120
tcagttctgc	tagtatagcg	tgaaagcagc	tatacacaat	acagaaatga	atgagtgtgg	1180
ttatgttcta	ataaaactta	tttataaaaa	caaggggagg	ctgggttttag	cctgtggggc	1240
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ataatcacat	tgcctttgtg	ttaatagtca	aatacttacc	tttgagaaat	acttaccttt	1420
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tgcactgggtg	acagacaaaa	tctgttttaa	aatcatatcc	agcacaaaaa	ctatttctgg	1900
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caaactgttt	tgaatggaag	gacaagtaag	agtgaggcca	cagttcccac	cacacgaggg	2020
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gccatgtata	agttgggcta	ttagagttca	tggaacatag	aacaaccatg	aatgagtggc	2140
atgatccgtg	cttaatgatc	aagtgttact	tatctaataa	tcctctagaa	agaaccctgt	2200
tagatcttgg	tttgtgataa	aaatataaag	acagaagaca	tgaggaaaaa	caaaagggtt	2260
gaggaaatca	ggcatatgac	tttataacta	acatcagatc	ttttctataa	tatcctacta	2320
ctttggtttt	cctagctcca	taccacacac	ctaaacctgt	attatgaatt	acatattaca	2380
aagtcataaa	tgtgccatat	ggatatacag	tacattctag	ttggaatcgt	ttactctgct	2440

61835-3.ST25.txt

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agaatttagg tgtgagattt tttgtttccc aggtatagca ggcttatggt tgggtggcatt 2500
aaattggttt ctttaaaatg ctttggtggc acttttgtaa acagattgct tctagattgt 2560
tacaaaccaa gcctaagaca catctgtgaa tacttagatt tgtagcttaa tcacattcta 2620
gacttgtgag ttgaatgaca aagcagttga acaaaaatta tggcatttaa gaatttaaca 2680
tgtcttagct gtaaaaatga gaaagtgttg gttggtttta aaatctggta actccatgat 2740
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aaaaaaaaa 2808

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<210> 50
<211> 176
<212> PRT
<213> homo sapiens

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<400> 50

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Met Ser Ala Gly Gly Ala Ser Val Pro Pro Pro Pro Asn Pro Ala Val
1          5          10          15

```

```

Ser Phe Pro Pro Pro Arg Val Thr Leu Pro Ala Gly Pro Asp Ile Leu
          20          25          30

```

```

Arg Thr Tyr Ser Gly Ala Phe Val Cys Leu Glu Ile Leu Phe Gly Gly
          35          40          45

```

```

Leu Val Trp Ile Leu Val Ala Ser Ser Asn Val Pro Leu Pro Leu Leu
          50          55          60

```

```

Gln Gly Trp Val Met Phe Val Ser Val Thr Ala Phe Phe Phe Ser Leu
65          70          75          80

```

```

Leu Phe Leu Gly Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala
          85          90          95

```

```

Asn Trp Asn Phe Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe
          100          105          110

```

```

Tyr Phe Gly Ala Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp
          115          120          125

```

```

Leu His Cys Asn Thr Thr Ile Thr Gly Gln Pro Leu Leu Ser Asp Asn
          130          135          140

```

61835-3.ST25.txt

Gln Tyr Asn Ile Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr
 145 150 155 160

Ala Cys Tyr Gly Cys Ser Leu Gly Leu Ala Leu Arg Arg Trp Arg Pro
 165 170 175

<210> 51
 <211> 3097
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (187)..(1575)

<400> 51
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 gaaccaaggg caactaaagc cgtcaggttc tgaacagctg gtagatgggc tggcttactg 180
 aaggac atg att cag act gtc ccg gac cca gca gct cat atc aag gaa 228
 Met Ile Gln Thr Val Pro Asp Pro Ala Ala His Ile Lys Glu
 1 5 10
 gcc tta tca gtt gtg agt gag gac cag tcg ttg ttt gag tgt gcc tac 276
 Ala Leu Ser Val Val Ser Glu Asp Gln Ser Leu Phe Glu Cys Ala Tyr
 15 20 25 30
 gga acg cca cac ctg gct aag aca gag atg acc gcg tcc tcc tcc agc 324
 Gly Thr Pro His Leu Ala Lys Thr Glu Met Thr Ala Ser Ser Ser Ser
 35 40 45
 gac tat gga cag act tcc aag atg agc cca cgc gtc cct cag cag gat 372
 Asp Tyr Gly Gln Thr Ser Lys Met Ser Pro Arg Val Pro Gln Gln Asp
 50 55 60
 tgg ctg tct caa ccc cca gcc agg gtc acc atc aaa atg gaa tgt aac 420
 Trp Leu Ser Gln Pro Pro Ala Arg Val Thr Ile Lys Met Glu Cys Asn
 65 70 75
 cct agc cag gtg aat ggc tca agg aac tct cct gat gaa tgc agt gtg 468
 Pro Ser Gln Val Asn Gly Ser Arg Asn Ser Pro Asp Glu Cys Ser Val
 80 85 90
 gcc aaa ggc ggg aag atg gtg ggc agc cca gac acc gtt ggg atg aac 516
 Ala Lys Gly Gly Lys Met Val Gly Ser Pro Asp Thr Val Gly Met Asn
 95 100 105 110
 tac ggc agc tac atg gag gag aag cac atg cca ccc cca aac atg acc 564
 Tyr Gly Ser Tyr Met Glu Glu Lys His Met Pro Pro Pro Asn Met Thr
 115 120 125
 acg aac gag cgc aga gtt atc gtg cca gca gat cct acg cta tgg agt 612
 Thr Asn Glu Arg Arg Val Ile Val Pro Ala Asp Pro Thr Leu Trp Ser

61835-3.ST25.txt

130										135										140										
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Thr	Asp	His	Val	Arg	Gln	Trp	Leu	Glu	Trp	Ala	Val	Lys	Glu	Tyr	Gly															
145										155																				
ctt	cca	gac	gtc	aac	atc	ttg	tta	ttc	cag	aac	atc	gat	ggg	aag	gaa	708														
Leu	Pro	Asp	Val	Asn	Ile	Leu	Leu	Phe	Gln	Asn	Ile	Asp	Gly	Lys	Glu															
160										170																				
ctg	tgc	aag	atg	acc	aag	gac	gac	ttc	cag	agg	ctc	acc	ccc	agc	tac	756														
Leu	Cys	Lys	Met	Thr	Lys	Asp	Asp	Phe	Gln	Arg	Leu	Thr	Pro	Ser	Tyr															
175										185																				
aac	gcc	gac	atc	ctt	ctc	tca	cat	ctc	cac	tac	ctc	aga	gag	act	cct	804														
Asn	Ala	Asp	Ile	Leu	Leu	Ser	His	Leu	His	Tyr	Leu	Arg	Glu	Thr	Pro															
195										205																				
ctt	cca	cat	ttg	act	tca	gat	gat	gtt	gat	aaa	gcc	tta	caa	aac	tct	852														
Leu	Pro	His	Leu	Thr	Ser	Asp	Asp	Val	Asp	Lys	Ala	Leu	Gln	Asn	Ser															
210										220																				
cca	cgg	tta	atg	cat	gct	aga	aac	aca	gat	tta	cca	tat	gag	ccc	ccc	900														
Pro	Arg	Leu	Met	His	Ala	Arg	Asn	Thr	Asp	Leu	Pro	Tyr	Glu	Pro	Pro															
225										235																				
agg	aga	tca	gcc	tgg	acc	ggt	cac	ggc	cac	ccc	acg	ccc	cag	tcg	aaa	948														
Arg	Arg	Ser	Ala	Trp	Thr	Gly	His	Gly	His	Pro	Thr	Pro	Gln	Ser	Lys															
240										250																				
gct	gct	caa	cca	tct	cct	tcc	aca	gtg	ccc	aaa	act	gaa	gac	cag	cgt	996														
Ala	Ala	Gln	Pro	Ser	Pro	Ser	Thr	Val	Pro	Lys	Thr	Glu	Asp	Gln	Arg															
255										265																				
cct	cag	tta	gat	cct	tat	cag	att	ctt	gga	cca	aca	agt	agc	cgc	ctt	1044														
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275										285																				
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Ala	Asn	Pro	Gly	Ser	Gly	Gln	Ile	Gln	Leu	Trp	Gln	Phe	Leu	Leu	Glu															
290										300																				
ctc	ctg	tcg	gac	agc	tcc	aac	tcc	agc	tgc	atc	acc	tgg	gaa	ggc	acc	1140														
Leu	Leu	Ser	Asp	Ser	Ser	Asn	Ser	Ser	Cys	Ile	Thr	Trp	Glu	Gly	Thr															
305										315																				
aac	ggg	gag	ttc	aag	atg	acg	gat	ccc	gac	gag	gtg	gcc	cgg	cgc	tgg	1188														
Asn	Gly	Glu	Phe	Lys	Met	Thr	Asp	Pro	Asp	Glu	Val	Ala	Arg	Arg	Trp															
320										330																				
gga	gag	cgg	aag	agc	aaa	ccc	aac	atg	aac	tac	gat	aag	ctc	agc	cgc	1236														
Gly	Glu	Arg	Lys	Ser	Lys	Pro	Asn	Met	Asn	Tyr	Asp	Lys	Leu	Ser	Arg															
335										345																				
gcc	ctc	cgt	tac	tac	tat	gac	aag	aac	atc	atg	acc	aag	gtc	cat	ggg	1284														
Ala	Leu	Arg	Tyr	Tyr	Tyr	Asp	Lys	Asn	Ile	Met	Thr	Lys	Val	His	Gly															
355										365																				
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61835-3.ST25.txt

Lys	Arg	Tyr	Ala	Tyr	Lys	Phe	Asp	Phe	His	Gly	Ile	Ala	Gln	Ala	Leu	
			370					375					380			
cag	ccc	cac	ccc	ccg	gag	tca	tct	ctg	tac	aag	tac	ccc	tca	gac	ctc	1380
Gln	Pro	His	Pro	Pro	Glu	Ser	Ser	Leu	Tyr	Lys	Tyr	Pro	Ser	Asp	Leu	
		385					390					395				
ccg	tac	atg	ggc	tcc	tat	cac	gcc	cac	cca	cag	aag	atg	aac	ttt	gtg	1428
Pro	Tyr	Met	Gly	Ser	Tyr	His	Ala	His	Pro	Gln	Lys	Met	Asn	Phe	Val	
	400					405					410					
gcg	ccc	cac	cct	cca	gcc	ctc	ccc	gtg	aca	tct	tcc	agt	ttt	ttt	gct	1476
Ala	Pro	His	Pro	Pro	Ala	Leu	Pro	Val	Thr	Ser	Ser	Ser	Phe	Phe	Ala	
415					420					425					430	
gcc	cca	aac	cca	tac	tgg	aat	tca	cca	act	ggg	ggg	ata	tac	ccc	aac	1524
Ala	Pro	Asn	Pro	Tyr	Trp	Asn	Ser	Pro	Thr	Gly	Gly	Ile	Tyr	Pro	Asn	
			435					440						445		
act	agg	ctc	ccc	acc	agc	cat	atg	cct	tct	cat	ctg	ggc	act	tac	tac	1572
Thr	Arg	Leu	Pro	Thr	Ser	His	Met	Pro	Ser	His	Leu	Gly	Thr	Tyr	Tyr	
		450						455				460				
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61835-3.ST25.txt

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Pro His Leu Ala Lys Thr Glu Met Thr Ala Ser Ser Ser Ser Asp Tyr
 35 40 45

Gly Gln Thr Ser Lys Met Ser Pro Arg Val Pro Gln Gln Asp Trp Leu
 50 55 60

Ser Gln Pro Pro Ala Arg Val Thr Ile Lys Met Glu Cys Asn Pro Ser
 65 70 75 80

Gln Val Asn Gly Ser Arg Asn Ser Pro Asp Glu Cys Ser Val Ala Lys
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Gly Gly Lys Met Val Gly Ser Pro Asp Thr Val Gly Met Asn Tyr Gly
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Ser Tyr Met Glu Glu Lys His Met Pro Pro Pro Asn Met Thr Thr Asn
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Glu Arg Arg Val Ile Val Pro Ala Asp Pro Thr Leu Trp Ser Thr Asp
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His Val Arg Gln Trp Leu Glu Trp Ala Val Lys Glu Tyr Gly Leu Pro
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 Asp Val Asn Ile Leu Leu Phe Gln Asn Ile Asp Gly Lys Glu Leu Cys
 165 170 175
 Lys Met Thr Lys Asp Asp Phe Gln Arg Leu Thr Pro Ser Tyr Asn Ala
 180 185 190
 Asp Ile Leu Leu Ser His Leu His Tyr Leu Arg Glu Thr Pro Leu Pro
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 His Leu Thr Ser Asp Asp Val Asp Lys Ala Leu Gln Asn Ser Pro Arg
 210 215 220
 Leu Met His Ala Arg Asn Thr Asp Leu Pro Tyr Glu Pro Pro Arg Arg
 225 230 235 240
 Ser Ala Trp Thr Gly His Gly His Pro Thr Pro Gln Ser Lys Ala Ala
 245 250 255
 Gln Pro Ser Pro Ser Thr Val Pro Lys Thr Glu Asp Gln Arg Pro Gln
 260 265 270
 Leu Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser Ser Arg Leu Ala Asn
 275 280 285
 Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu Leu
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 Ser Asp Ser Ser Asn Ser Ser Cys Ile Thr Trp Glu Gly Thr Asn Gly
 305 310 315 320
 Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg Trp Gly Glu
 325 330 335
 Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser Arg Ala Leu
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 Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His Gly Lys Arg
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 Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln Ala Leu Gln Pro
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His Pro Pro Glu Ser Ser Leu Tyr Lys Tyr Pro Ser Asp Leu Pro Tyr
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Met Gly Ser Tyr His Ala His Pro Gln Lys Met Asn Phe Val Ala Pro
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His Pro Pro Ala Leu Pro Val Thr Ser Ser Ser Phe Phe Ala Ala Pro
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Asn Pro Tyr Trp Asn Ser Pro Thr Gly Gly Ile Tyr Pro Asn Thr Arg
435 440 445

Leu Pro Thr Ser His Met Pro Ser His Leu Gly Thr Tyr Tyr
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